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OM protein - protein search, using sw model

Run on: August 21, 2002, 15:25:51 ; Search time 29.23 Seconds

(without alignments)  
34.200 Million cell updates/sec

Title: US-09-633-364-6827

Perfect score: 1 VLAKEKRV 9

Sequence: BLOSUM62

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 11107396 residues

Total number of hits satisfying chosen parameters: 194182

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:\*  
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:\*  
5: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:\*  
6: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:\*  
7: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:\*  
8: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:\*  
9: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:\*  
10: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:\*  
11: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:\*  
12: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:\*  
13: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:\*  
14: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:\*  
15: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:\*  
16: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:\*  
17: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:\*  
18: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:\*  
19: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:\*  
20: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:\*  
21: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	9	15	AA73864
2	41	100.0	9	21	AA72836
3	41	100.0	9	22	AAU06387
4	41	100.0	9	22	AAU06424
5	41	100.0	10	22	AAU06426
6	41	100.0	11	22	AAU06425
7	38	92.7	10	22	AAU06423
8	37	90.2	9	22	AAU06372
9	31	75.6	9	20	AA446778
10	31	75.6	15	17	AAW05203
11	28	68.3	8	12	AA14165

12	27	65.9	8	19	AAW69677	Helicobacter pylori
13	27	65.9	14	20	AAZ28976	Antimicrobial pept
14	27	65.9	14	20	AAZ28967	Antimicrobial pept
15	27	65.9	14	21	AAI13937	Type 1 antiviral p
16	27	65.9	14	21	AAI13946	Antiviral peptide
17	27	65.9	14	21	AAV77081	Antimicrobial pept
18	27	65.9	14	21	AAV77090	Antimicrobial pept
19	27	65.9	14	21	AAV50850	Antifungal peptide
20	27	65.9	14	21	AAV50859	Antifungal peptide
21	27	65.9	14	21	AAV50864	Antifungal peptide
22	27	65.9	14	22	AAU07797	Human histatin 5 c
23	27	65.9	15	20	AAZ28981	Antimicrobial pept
24	27	65.9	15	21	AAV68620	Antimicrobial pept
25	26	63.4	10	15	AA64030	Haematopoiesis inh
26	25	61.0	8	21	AAV68620	Antimicrobial pept
27	25	61.0	14	22	AAU00147	Amino acid sequenc
28	25	61.0	14	22	AAU00148	Human protein frag
29	25	61.0	14	22	AAU00149	Human protein frag
30	24	58.5	8	12	AAI13462	pe-Glu246, 247, 24
31	24	58.5	9	20	AA659052	Pseudomonas aerugi
32	24	58.5	8	22	AA659052	Immunogenic peptid
33	24	58.5	12	17	AAI46693	Immunogenic peptid
34	24	58.5	14	22	AAV77178	Human peptide #452
35	24	58.5	14	22	AAV77178	Human peptide #453
36	23	56.1	5	17	AA886894	Allergen Alt a 45
37	23	56.1	7	18	AAW31013	Timothy grass poll
38	23	56.1	7	22	AAU46602	HII binding site c
39	23	56.1	9	22	AAU06378	Human Leukocyte An
40	23	56.1	10	22	AA686588	Saccharomyces cere
41	23	56.1	14	20	AAZ28973	Antimicrobial pept
42	23	56.1	14	21	AAI13943	Type 1 antiviral p
43	23	56.1	14	21	AAV77087	Antimicrobial pept
44	23	56.1	14	21	AAV50856	Antifungal peptide
45	23	56.1	14	21	AAV50865	Antifungal peptide

#### ALIGNMENTS

RESULT 1  
ID AAR73864 standard; peptide: 9 AA.  
AC AAR73864:  
XX 22-JUN-1995 (first entry)  
XX  
DE Antigen fragment 180, from PAP has binding affinity for HLA-2.1.  
XX  
KW antigen; epitope; immunogenic target protein; PSN; HRYC; HBVS; EBV;  
KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;  
KW human immunodeficiency virus; human papilloma virus; p53; c-erbB2;  
KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;  
KW pharmaceutical composition; in vivo; ex vivo; therapeutic;  
KW diagnostic; MHC class I molecule; major histocompatibility complex;  
KW HLA-A2.1; pmer; lomer; anchor; human leukocyte antigen; PLP; dmer;  
KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;  
KW herpes simplex virus; influenza A; M1; LCMV; PAP.  
XX  
OS Synthetic.  
XX  
XX W09420127-A.  
XX PN  
XX 15-SEP-1994.  
XX PD  
XX  
XX 04-MAR-1994; 94WO-US02353.  
XX PF  
XX  
XX 05-MAR-1993; 93US-0027146.  
XX PR  
XX 04-JUN-1993; 93US-0073205.  
XX PR  
XX 29-NOV-1993; 93US-0159184.  
XX  
XX  
XX (CYTE-) CYTEL CORP.

PI Grey HM, Kast WM, Sette A, Sidney J;  
 XX WPI; 1994-302678/37.  
 DR  
 XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used  
 PT for treatment or prophylaxis of cancer, virus infection or  
 PT autoimmune diseases.  
 PS  
 XX Disclosure; Page 87; 138pp; English.  
 CC AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using  
 CC motifs disclosed in the invention, these peptides were screened for  
 CC further motifs. Only peptides with binding affinity of at least 18  
 CC (binding affinity is expressed as an IC50 value) as compared to the  
 CC standard peptide (AAR71293) in assays. This peptide from PAP (SIC) has a  
 CC binding value of 0.0590. The peptides of the invention can induce  
 CC cytotoxic T lymphocytes which can react with target cells. They can  
 CC be used for the treatment or prophylaxis of cancer, eg. prostate  
 CC cancer or lymphoma, etc.  
 CC  
 XX Sequence 9 AA:  
 SQ  
 Query Match 100.0%; Score 41; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLAKEIKFV 9  
 DB 1.vlakeikfv 9  
 RESULT 2  
 ID AAY82836 standard; peptide: 9 AA.  
 XX AAY82836;  
 AC  
 XX 19-JUN-2000 (first entry)  
 DT  
 XX Prostate acid phosphatase fragment (tumour associated antigen).  
 DE  
 XX Tumour associated antigen peptide; TAA; cancer: carcinoma;  
 KW treatment; prevention; cure; anti-tumour vaccine; metastases;  
 KW breast; bladder; prostate; pancreas; ovary; thyroid; colon;  
 KW stomach; carcinoma; MHC Class I; HLA-A2; human;  
 KW Major Histocompatibility Complex; uroplakin;  
 KW prostate specific antigen; prostate specific membrane antigen;  
 KW prostate acid phosphatase; mucin; lactadherin;  
 KW teratocarcinoma derived growth factor; PSA; PSMA; PAP; CRIPTO-1.  
 KW  
 XX Homo sapiens.  
 OS  
 XX MO200006723-A1.  
 PN  
 XX 10-FEB-2000.  
 PD  
 XX 29-JUL-1999; 99MO-IL00417.  
 PF  
 XX 30-JUL-1998; 98IL-0125608.  
 PR  
 XX (YEDA ) YEDA RES & DEV CO LTD.  
 PA (BIO-) BIO-TECHNOLOGY GEN CORP.  
 PI Eisenbach L, Garmon L, Tirosh B, Bar-haim E, Paz A, Fridkin M;  
 XX Filtzer-atlas C;  
 XX WPI; 2000-205463/18.  
 DR  
 XX Tumour associated antigen peptides, especially derived from uroplakin,  
 PT useful as vaccines to prevent or cure cancers including breast,  
 PT bladder, prostate, pancreas, ovary, thyroid, colon and stomach -  
 XX

PS Claim 10; Page 98; 113pp; English.  
 XX  
 XX Tumour associated antigen peptides (TAA) may be used for the  
 CC treatment, prevention and cure of cancer or cancer metastases. The  
 CC cancer may be breast, bladder, prostate, pancreas, ovary, thyroid,  
 CC colon, stomach, head or neck cancer or a carcinoma. The tumour  
 CC associated antigens are presentable to the immune system by HLA-A2  
 CC molecules and are generally between 8 to 10 amino acids in length.  
 CC The amino acids located at positions 2 and 9 of the tumour associated  
 CC antigens are the anchor residues which participate in the binding to  
 CC MHC class I molecules, more specifically HLA-A2. More tumour  
 CC associated antigens are described in records AAY82806-Y82882.  
 CC Those tumour associated antigens described in records AAY82806-Y82824  
 CC and AAY82855-Y82869 are derived from uroplakin, such as uroplakin II,  
 CC uroplakin Ia, uroplakin III and uroplakin Ib. Those described in  
 CC records AAY82825-Y82829 are derived from prostate specific antigen  
 CC (PSA). Those described in records AAY82830-Y82835 are derived from  
 CC prostate specific membrane antigen (PSMA). Those described in  
 CC records Y82836-AAY82839 are derived from prostate acid phosphatase  
 CC (PAP). Those described in records AAY82840-Y82846 are derived  
 CC from lactadherin (Ba-46). Those described in records AAY82847-Y82854  
 CC are derived from Mucin and those described in records AAY82871-Y82882  
 CC are derived from Teratocarcinoma derived growth factor (CRIPTO-1).  
 CC  
 XX Sequence 9 AA:  
 SQ  
 Query Match 100.0%; Score 41; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLAKEIKFV 9  
 DB 1.vlakeikfv 9  
 RESULT 3  
 ID AAU06387 standard; Peptide: 9 AA.  
 XX AAU06387;  
 AC  
 XX 24-OCT-2001 (first entry)  
 DT  
 XX Human prostate antigen binding peptide #9.  
 DE  
 XX Prostate cancer-associated antigen; supermotif; human leukocyte antigen;  
 KW HLA; cytotoxic T lymphocyte; helper T lymphocyte; HLA superfamily; CTL;  
 KW Immunogenecity; Immunosuppression; HTL.  
 KW  
 XX Homo sapiens.  
 OS  
 XX MO200145728-A2.  
 PN  
 XX 28-JUN-2001.  
 PD  
 XX 20-DEC-2000; 2000MO-US35516.  
 PE  
 XX 21-DEC-1999; 99US-0171312.  
 PR 07-AUG-2000; 2000US-0633364.  
 XX (EPIM-) EPIMUNE INC.  
 PA Pikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
 PI Keogh E;  
 XX WPI; 2001-398311/42.  
 DR  
 XX Tumour antigen-associated group-based vaccines useful for vaccinating  
 PT against prostate cancer -  
 PT Example 2; Page 237; 252pp; English.  
 PS



SQ Sequence 10 AA:

Query Match 100.0%; Score 41; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.051;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLAKELKFV 9  
 :|||||  
 Db 1 vlakelkf 9

## RESULT 6

AAU06425 standard; Peptide: 11 AA.

AC AAU06425:

DT 24-OCT-2001 (first entry)

DE Human Leukocyte Antigen-A2 (HLA-A2) supermotif binding peptide #17.

XX Prostate cancer-associated antigen: supermotif; human leukocyte antigen;

KW HLA: cytotoxic T lymphocyte helper T lymphocyte; HLA superfamily; CTL;

KM Immunogenicity; Immunosuppression; HTL.

OS Homo sapiens.

PN WO200145728-A2.

PD 28-JUN-2001.

PF 20-DEC-2000; 2000WO-US35516.

PR 21-DEC-1999; 99US-0171312.

PR 07-AUG-2000; 2000US-0633364.

XX (EPIM-) EPIMUNE INC.

XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;

PI Keogh E;

PT Tumour antigen-associated group-based vaccines useful for vaccinating

PT against prostate cancer -

PS Example 2; Page 238; 252pp; English.

CC The sequences represent prostate cancer-associated antigens and derived

CC motif or supermotif epitopes. The peptide epitopes are included in

CC prostate cancer vaccine compositions due to their ability to bind to

CC human leukocyte antigen (HLA) molecules, which recognise the motifs.

CC Peptides with a high binding affinity are further tested for their

CC ability to induce a cytotoxic T lymphocyte (CTL) or a helper T lymphocyte

CC (HTL) response. Supermotif-bearing peptides may also be tested for their

CC binding affinity to multiple alleles within the HLA superfamily. The

CC vaccine compositions can be modified, for example, to enhance

CC immunogenicity, to avoid the inclusion of immunosuppressive groups, or to

CC alter the immune response to suit the target disease. These group-based

CC vaccines allow the focus of an immune response to multiple selected

CC antigens from the same pathogen. Variability among the immune responses

CC of patients can therefore be alleviated by the inclusion of groups from

CC multiple antigens in a vaccine.

SQ Sequence 11 AA:

Query Match 100.0%; Score 41; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.057;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLAKELKFV 9

Db :|||||  
 1 vlakelkf 9

## RESULT 7

AAU06423 standard; Peptide: 10 AA.

AC AAU06423:

DT 24-OCT-2001 (first entry)

DE Human Leukocyte Antigen-A2 (HLA-A2) supermotif binding peptide #15.

XX Prostate cancer-associated antigen: supermotif; human leukocyte antigen;

KW HLA: cytotoxic T lymphocyte helper T lymphocyte; HLA superfamily; CTL;

KM Immunogenicity; Immunosuppression; HTL.

OS Homo sapiens.

PN WO200145728-A2.

PD 28-JUN-2001.

PF 20-DEC-2000; 2000WO-US35516.

PR 21-DEC-1999; 99US-0171312.

PR 07-AUG-2000; 2000US-0633364.

XX (EPIM-) EPIMUNE INC.

XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;

PI Keogh E;

PT Tumour antigen-associated group-based vaccines useful for vaccinating

PT against prostate cancer -

PS Example 2; Page 238; 252pp; English.

CC The sequences represent prostate cancer-associated antigens and derived

CC motif or supermotif epitopes. The peptide epitopes are included in

CC prostate cancer vaccine compositions due to their ability to bind to

CC human leukocyte antigen (HLA) molecules, which recognise the motifs.

CC Peptides with a high binding affinity are further tested for their

CC ability to induce a cytotoxic T lymphocyte (CTL) or a helper T lymphocyte

CC (HTL) response. Supermotif-bearing peptides may also be tested for their

CC binding affinity to multiple alleles within the HLA superfamily. The

CC vaccine compositions can be modified, for example, to enhance

CC immunogenicity, to avoid the inclusion of immunosuppressive groups, or to

CC alter the immune response to suit the target disease. These group-based

CC vaccines allow the focus of an immune response to multiple selected

CC antigens from the same pathogen. Variability among the immune responses

CC of patients can therefore be alleviated by the inclusion of groups from

CC multiple antigens in a vaccine.

SQ Sequence 10 AA:

Query Match 92.7%; Score 38; DB 22; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 0.21;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

OY 1 VLAKELKFV 9  
 :|||||  
 Db 2 llakelkf 10

RESULT 8  
 AAU06372 standard; Peptide: 9 AA.

AC	AA06372:
XX	
DT	24-OCT-2001 (first entry)
DE	Human Leukocyte Antigen-DP3b (HLA-DP3b) submotif peptide epitope #14.
XX	
XX	
XX	Prostate cancer-associated antigen; supermotif; human leukocyte antigen;
KM	HLA: cytotoxic T lymphocyte; helper T lymphocyte; HLA superfamily; CTL;
KW	immunogenicity; immunosuppression; HTL.
XX	
OS	Homo sapiens.
PX	
PN	M0200145728-A2.
PD	
PD	28-JUN-2001.
PF	
PF	20-DEC-2000; 2000MO-US35516.
PR	
PR	21-DEC-1999; 990S-0171312.
PR	07-AUG-2000; 2000US-0633364.
PA	(EPI-M-) EPIMUNE INC.
PI	
PI	Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;
PI	Keogh E;
DR	WPI; 2001-398311/42.
XX	
PT	Tumour antigen-associated group-based vaccines useful for vaccinating
PT	against prostate cancer -
PS	
PS	Example 5; Page 235; 252pp; English.
CC	The sequences represent prostate cancer-associated antigens and derived
CC	motif or supermotif epitopes. The peptide epitopes are included in
CC	prostate cancer vaccine compositions due to their ability to bind to
CC	human leukocyte antigen (HLA) molecules, which recognise the motifs.
CC	Peptides with a high binding affinity are further tested for their
CC	ability to induce a cytotoxic T lymphocyte (CTL) or a helper T lymphocyte
CC	(HTL) response. Supermotif-bearing peptides may also be tested for their
CC	binding affinity to multiple alleles within the HLA superfamily. The
CC	vaccine compositions can be modified, for example, to enhance
CC	immunogenicity, to avoid the inclusion of immunosuppressive groups, or to
CC	alter the immune response to suit the target disease. These group-based
CC	vaccines allow the focus of an immune response to multiple selected
CC	antigens from the same pathogen. Variability among the immune responses
CC	of patients can therefore be alleviated by the inclusion of groups from
CC	multiple antigens in a vaccine.
XX	
SQ	Sequence 9 AA:
Query Match	90.2%; Score 37; DB 22; Length 9;
Best Local Similarity	100.0%; Pred. No. 6.4e+05;
Matches 8; Conservative	0; Mismatches 0; Indels 0; Gaps 0.
Oy	2 LAKELEFV 9               1 lakelefv 8
Dd	
RESULT 9	
ID	AA146778
ID	AA146778 standard; Peptide: 9 AA.
XX	
MC	AA146778:
DT	01-DEC-1999 (first entry)
XX	
DE	Immunogenic peptide having a human leukocyte antigen binding motif #1389.
XX	
KM	Human leukocyte antigen: binding; immunogenic; glycoprotein; MIC; HLA;
KW	immune response; T cell activation; major histocompatibility complex;

KM cytotoxic T lymphocytes; CTL; tumour rejection; viral infection; cancer;  
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
XX vaccine; immunisation.

OS Synthetic.  
OS Homo sapiens.  
PN MO9849954-A1.  
PX 16-SEP-1999.  
PD  
PE 13-MAR-1998; 98MO-US05039.  
PF 13-MAR-1998; 98MO-US05039.  
PI (EPM-) EPIMONE INC.  
PA Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;  
FI WPI: 1999-551214/46.  
DR  
XX New immunogenic peptides with HLA binding motif, useful in treatment  
PT and diagnosis of cancers and viral diseases -  
PS  
XX Claim 1: Page 84; 150pp: English.

CC AA45390 to AA478214 represent specifically claimed immunogenic peptides  
CC known as human major histocompatibility complex (MHC) Class I (also  
CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic  
CC peptides can bind to a specific HLA allele (I.e. HLA-A subtypes  
CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell  
CC response against the antigen from which the peptide is derived.  
CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are  
CC normally induced by an antigen in the form of a peptide fragment bound  
CC to a HLA molecule, rather than the intact foreign antigen itself, and  
CC are particularly important in tumour rejection and in fighting viral  
CC infections. The peptides are therefore useful therapeutically to treat  
CC or prevent vital infections and cancers in mammals (especially humans)  
CC e.g. prostatic cancer, hepatitis B and C, AIDS, and renal carcinoma.  
CC They can be administered as vaccines to elicit an immune response in  
CC individuals susceptible or otherwise at risk of viral infection or  
CC cancer, or used to treat chronic or acute conditions. They are also  
CC useful diagnostically, and can be used to induce a cytotoxic T cell  
CC response, by contacting a cytotoxic T cell with the peptide e.g., to  
CC produce CTLs ex vivo for infusion back into a patient. The  
CC polynucleotides encoding the immunogenic peptides are also useful  
CC therapeutically and for immunisation as above.

SQ Sequence 9 AA:

Query Match 75.6%, Score 31: DB 20: Length 9:  
Best Local Similarity 100.0%; Pred.No. 6;4+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 VIANELK 7  
| | | | | |  
Db 3 vianelk 9

RESULT 10  
AAW05203 standard; Peptide; 15 AA.  
AC AAW05203;  
DE 31-JUN-1997 (first entry)

XX Helicobacter Family F (Hsp60) antigen N-terminal peptide.  
KM Antigen; vaccine; gastrointestinal disease; heat shock protein;  
HX hsp60.  
XX



XX Protein antigens from *Helicobacter pylori* and their antigenic  
 PT fragments - useful for diagnostic detection of specific antibodies  
 PT and for vaccination  
 PS  
 PS Example 1; Page 27; 47pp; English.  
 CC The present invention describes *Helicobacter pylori* antigens which are  
 CC of molecular weight (m.w.) 43-53 kDa, under denaturing and reducing  
 CC conditions. The present sequence represents a H. pylori antigenic  
 CC peptides from an example in the present invention. H. pylori antigens  
 CC and their fragments are used: (a) for diagnostic detection of H. pylori  
 CC by detection of specific immunoglobulin G antibodies, particularly in  
 CC saliva or blood, and (b) as vaccines for treating or preventing  
 CC H. pylori infection.  
 CC  
 SQ Sequence 8 AA;  
 Query Match 65.9%; Score 27; DB 19; Length 8;  
 Best Local Similarity 83.3%; Pred. No. 6,4e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 AKELKF 8  
 DB 1 AKELKF 6  
 RESULT 13  
 ID AAY28976 standard; peptide: 14 AA.  
 AC AAY28976;  
 DT 04-OCT-1999 (first entry)  
 DE Antimicrobial peptide 12.  
 KW Antimicrobial: histatin 5; bacterial; fungal; yeast infection;  
 KM salivary peptide.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Modified-site 14  
 FT note- "C-terminal amide"  
 PN MO9937678-A2.  
 PD 29-JUL-1999.  
 PF 26-JAN-1999; 99MO-NL00045.  
 PR 27-JAN-1998; 98NL-1008139.  
 PS (TEME-) STICHTING TECH WETENSCHAPPEN.  
 PI Helmerhorst EJ, Van Nieuw Amerongen A, Van't Hof W;  
 PI Veerman ECI;  
 DR WPI: 1999-469115/39.  
 PT New antimicrobial peptides with two domains containing mostly  
 PT positively charged or unchanged amino acids, e.g. for treating  
 PT bacterial or fungal infections  
 CC Example 2; Page 9; 28pp; English.  
 CC The invention relates to antimicrobial peptides containing a domain of  
 CC 10-25 aa in which most aa in one half are positively charged, while most  
 CC in the other half are unchanged. These antimicrobial peptides are  
 CC synthesised by modifying the C-terminal sequence of histatin 5 peptide.  
 CC The peptides are used to treat bacterial, fungal or yeast infections  
 CC on the skin, in cattle and in foods. These antimicrobial peptides are  
 CC more active than natural salivary peptides (e.g. histatin) and are less  
 CC subject to proteolysis and, being rather small, can be produced  
 CC relatively inexpensively. They have practically no hemolytic action.  
 CC The present sequence represents a specific example of the antimicrobial  
 CC peptide of the invention.

CC Typical applications are control of *Candida* and of bacteria in the mouth,  
 CC on the skin, in cattle and in foods. These antimicrobial peptides are  
 CC more active than natural salivary peptides (e.g. histatin) and are less  
 CC subject to proteolysis and, being rather small, can be produced  
 CC relatively inexpensively. They have practically no hemolytic action.  
 CC The present sequence represents an example of an antimicrobial peptide.  
 CC  
 SQ Sequence 14 AA;  
 Query Match 65.9%; Score 27; DB 20; Length 14;  
 Best Local Similarity 85.7%; Pred. No. 52;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LAELKF 8  
 DB 3 lfeLKF 9  
 RESULT 14  
 ID AAY28967 standard; peptide: 14 AA.  
 AC AAY28967;  
 DT 04-OCT-1999 (first entry)  
 DE Antimicrobial peptide 3.  
 KW Antimicrobial: histatin 5; bacterial; fungal; yeast infection;  
 KM salivary peptide.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Modified-site 14  
 FT note- "C-terminal amide"  
 PN MO9937678-A2.  
 PD 29-JUL-1999.  
 PF 26-JAN-1999; 99MO-NL00045.  
 PR 27-JAN-1998; 98NL-1008139.  
 PS (TEME-) STICHTING TECH WETENSCHAPPEN.  
 PI Helmerhorst EJ, Van Nieuw Amerongen A, Van't Hof W;  
 PI Veerman ECI;  
 DR WPI: 1999-469115/39.  
 PT New antimicrobial peptides with two domains containing mostly  
 PT positively charged or unchanged amino acids, e.g. for treating  
 PT bacterial or fungal infections  
 CC Claim 8; Page 19; 28pp; English.  
 CC The invention relates to antimicrobial peptides containing a domain of  
 CC 10-25 aa in which most aa in one half are positively charged, while most  
 CC in the other half are unchanged. These antimicrobial peptides are  
 CC synthesised by modifying the C-terminal sequence of histatin 5 peptide.  
 CC The peptides are used to treat bacterial, fungal or yeast infections  
 CC on the skin, in cattle and in foods. These antimicrobial peptides are  
 CC more active than natural salivary peptides (e.g. histatin) and are less  
 CC subject to proteolysis and, being rather small, can be produced  
 CC relatively inexpensively. They have practically no hemolytic action.  
 CC The present sequence represents a specific example of the antimicrobial  
 CC peptide of the invention.

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 LAKEKF 8  
| | | | |  
Db 3 lkeKf 9

## RESULT 15

AAB13937  
ID AAB13937 standard; peptide; 14 AA.

AC AAB13937;

DT 16-NOV-2000 (first entry)

DE Type 1 antiviral peptide #3.

KM Antiviral; antiulcer; human immunodeficiency virus; HIV;

KW herpes simplex virus; HSV; cold sore; aphthous ulcer;

XX viral bronchial infection.

XX Synthetic.

XX WO200032629-A2.

XX 08-JUN-2000.

XX 01-DEC-1999; 99WO-NL00732.

XX 01-DEC-1998; 98NL-1010692.

XX (TEME-) STICHTING TECH WETENSCHAPPEN.

XX Van Nieuw Amerongen A, Veerman ECI, Van 't Hof W, Nibbering PH;

XX WPI: 2000-412289/35.

XX Antiviral peptides comprising a domain of 10-25 amino acids, half of

XX which is positively charged and half unchanged, useful for treatment of

XX human immunodeficiency virus and herpes simplex virus -

XX Claim 13; Page 7; 20pp; English.

XX The present invention relates to antiviral peptides containing a domain

XX of 10-25 amino acids, where half the domain is positively charged and

XX the other half is unchanged. The present sequence is a type 1

XX antiviral peptide. Oligomers consisting of at least two peptides

XX coupled together are also included in the invention. The peptides are

XX useful for treating viral infections such as human immunodeficiency

XX virus (HIV) and herpes simplex virus (HSV) and for the treatment of

XX cold sores, aphthous ulcers and viral bronchial infections.

XX Sequence 14 AA:

Query Match 65.9%; Score 27; DB 21; Length 14;

Best Local Similarity 85.7%; Pred. No. 52;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 LAKEKF 8  
| | | | |  
Db 3 lkeKf 9

Search completed: August 21, 2002, 15:28:01  
Job time: 130 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 21, 2002, 15:26:11 ; Search time 13.02 seconds  
(without alignments)  
16,884 Million cell updates/sec

Title: US-09-633-364-6827

Perfect score: 41

Sequence: 1 VLAKELKVV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 101902

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued\_Patents\_AA: \*  
1: /cgn2.6/ptodata/2/1aa/5A.COMB.pep: \*  
2: /cgn2.6/ptodata/2/1aa/5B.COMB.pep: \*  
3: /cgn2.6/ptodata/2/1aa/6A.COMB.pep: \*  
4: /cgn2.6/ptodata/2/1aa/6B.COMB.pep: \*  
5: /cgn2.6/ptodata/2/1aa/PCtUS.COMB.pep: \*  
6: /cgn2.6/ptodata/2/1aa/Backt1last1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	68.3	8	1	US-08-467-264-19
2	27	65.9	8	2	US-08-467-822-9
3	27	65.9	8	4	US-08-432-697-9
4	27	65.9	8	4	US-08-466-248-9
5	26	63.4	10	1	US-08-284-477-2
6	24	58.5	8	1	US-08-467-264-15
7	24	58.5	12	1	US-08-319-590-11
8	24	58.5	12	1	US-08-487-001A-11
9	24	58.5	12	2	US-08-630-822A-11
10	24	58.5	12	2	US-08-711-905-11
11	24	58.5	12	2	US-09-005-069-11
12	24	58.5	12	2	US-09-465-325-131
13	24	58.5	11	4	US-09-115-737-131
14	24	58.5	12	3	US-08-498-346-10
15	24	58.5	12	4	US-08-311-611A-4
16	24	58.5	13	1	US-08-311-611A-5
17	24	58.5	13	1	US-08-312-783-4
18	24	58.5	15	1	US-08-312-783-5
19	24	58.5	15	1	US-08-312-783-5
20	24	58.5	15	1	US-08-312-783-5
21	24	58.5	15	1	US-08-312-783-5
22	24	58.5	15	1	US-08-312-783-5
23	24	58.5	15	1	US-08-312-783-5
24	24	58.5	15	1	US-08-312-783-5
25	24	58.5	15	1	US-08-312-783-5
26	24	58.5	15	1	US-08-312-783-5
27	24	58.5	15	1	US-08-312-783-5

28 22 53.7 15 1 US-08-473-344-5  
29 22 53.7 15 2 US-08-621-803-1  
30 22 53.7 15 2 US-08-621-803-55  
31 22 53.7 15 2 US-08-485-445A-4  
32 22 53.7 15 2 US-08-485-445A-5  
33 22 53.7 15 3 US-08-414-174-4  
34 22 53.7 15 3 US-09-119-263-4  
35 22 53.7 15 3 US-09-119-263-5  
36 22 53.7 15 4 US-08-657-162-4  
37 22 53.7 15 4 US-08-657-162-5  
38 22 53.7 15 4 US-09-224-480-5  
39 22 53.7 15 4 US-09-224-480-5  
40 22 53.7 15 4 US-09-093-539-4  
41 22 53.7 15 4 US-09-093-539-5  
42 22 53.7 15 4 US-09-217-352-1  
43 22 53.7 15 4 US-09-217-352-5  
44 22 53.7 15 5 PCT-US94-02465-4  
45 22 53.7 15 5 PCT-US94-02465-5

#### ALIGNMENTS

RESULT 1  
US-08-467-264-19  
Sequence 19, Application US/08467264  
Patent No. 5705156  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: FitzGerald, David  
TITLE OF INVENTION: Pseudomonas Exotoxins of Low Animal  
TITLE OF INVENTION: Cytotoxicity and High Cytocidal Activity  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/467,264  
APPLICATION NUMBER: 424  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/522,182  
FILING DATE: 11-MAY-1990  
PRIOR APPLICATION DATA: US 08/130,322  
APPLICATION NUMBER: 1993  
FILING DATE: 01-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 15280-125-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-467-264-19

Query Match 68.3%, Score 28, DB 1, Length 8;  
Best Local Similarity 62.5%, Pred. No. 1.7e+05;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLAKELKF 8  
DB 1 VISKIKLF 8

RESULT 2  
US-08-467-822-9

; Sequence 9, Application US/08467822  
; Patent No. 5843460

GENERAL INFORMATION:

APPLICANT: Labigne, Agnes

APPLICANT: Sauerbaum, Sebastien

APPLICANT: Ferrero, Richard L.

APPLICANT: Thibierge, Jean-Michel

TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST

TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE

TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID

TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS: 44

ADDRESS: Flunegan, Henderson, Farabow, Garrett &

ADDRESS: Dunnet

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,822

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/447,177

FILING DATE: 19-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/432,697

FILING DATE: 02-MAY-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03495, 0137-02000

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-467-822-9

Query Match 65.9%, Score 27, DB 2, Length 8;  
Best Local Similarity 83.3%, Pred. No. 1.7e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 AKELKF 8  
DB 1 AKELKF 6

RESULT 3  
US-08-432-697-9

; Sequence 9, Application US/08432697

; Patent No. 6248330

GENERAL INFORMATION:

APPLICANT: Labigne, Agnes

APPLICANT: Sauerbaum, Sebastien

APPLICANT: Ferrero, Richard L.

APPLICANT: Thibierge, Jean-Michel

TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST

TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE

TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID

TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS: 44

ADDRESS: Flunegan, Henderson, Farabow, Garrett &

ADDRESS: Dunnet

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/432,697

FILING DATE: 02-MAY-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03495, 0137-00000

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-432-697-9

Query Match 65.9%, Score 27, DB 4, Length 8;  
Best Local Similarity 83.3%, Pred. No. 1.7e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 AKELKF 8  
DB 1 AKELKF 6

RESULT 4  
US-08-466-248-9

; Sequence 9, Application US/08466248

; Patent No. 6258359

GENERAL INFORMATION:

APPLICANT: Labigne, Agnes

APPLICANT: Sauerbaum, Sebastien

APPLICANT: Ferrero, Richard L.

APPLICANT: Thibierge, Jean-Michel

TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST

TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE

TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID

TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS: 44

ADDRESS: Pinegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunne  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,248  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
APPLICATION NUMBER: 435  
FILING DATE: 19-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/447,177  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/432,697  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0137-02000  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4000  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-466-248-9

Query Match 65.9%; Score 27; DB 4; Length 8;  
Best Local Similarity 83.3%; Pred. No. 1.7e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 AKEKF 8  
Db 1 AKEKF 6

RESULT 5  
US-08-284-477-2  
Sequence 2, Application US/08284477  
Patent No. 5711881  
GENERAL INFORMATION:  
APPLICANT: Yanada, Satoko  
APPLICANT: Kataoka, Hiroshi  
TITLE OF INVENTION: HEMATOPOIETIC INHIBITING FACTOR  
TITLE OF INVENTION: CONTAINING COMPOSITIONS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 601 13th Street, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/284,477  
FILING DATE: 06-OCT-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Breischneider, Barry E.  
REGISTRATION NUMBER: 28,055  
REFERENCE/DOCKET NUMBER: 04477/050001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/783-5070  
TELEFAX: 202/783-2331  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-284-477-2

Query Match 63.4%; Score 26; DB 1; Length 10;  
Best Local Similarity 83.3%; Pred. No. 19;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

OY 3 AKEKF 8  
Db 2 AKEKF 7

RESULT 6  
US-08-467-264-15  
Sequence 15, Application US/08467264  
Patent No. 5705156  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: Fitzgerald, David  
APPLICANT: Chaudhary, Vijay K.  
TITLE OF INVENTION: Pseudomonas Exotoxins of Low Animal  
TITLE OF INVENTION: Cytotoxicity and High Cytocidal Activity  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,264  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION NUMBER: US 07/522,182  
FILING DATE: 11-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/130,322  
FILING DATE: 01-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 15280-125-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-467-264-15

Query Match 58.5%; Score 24; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.7e+05;  
Matches 4; Conservative 4; Mismatches 0; Indels 0;

QY 1 VLAKELF 8  
DB 1 VISELELF 8

RESULT 7  
US-08-319-590-11  
Sequence 11, Application US/08319590  
Patent No. 5646115  
GENERAL INFORMATION:  
APPLICANT: FRANK, GLENN R.  
APPLICANT: WU HUNTER, SHIRLEY  
APPLICANT: WALLENFELS, LYNDIA  
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND  
TITLE OF INVENTION: APPARATUS TO COLLECT SUCH PROTEINS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SHERIDAN ROSS & MCINTOSH  
STREET: 1700 LINCOLN ST., SUITE 3500  
CITY: DENVER  
STATE: CO  
COUNTRY: USA  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/319,590  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: VERSER, CAROL TALKINGTON  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: 2618-17  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/863-9700  
TELEFAX: 303/863-0223  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-319-590-11

Query Match 58.5%; Score 24; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 5 ELKVF 9  
DB 3 ELKVF 7

RESULT 8  
US-08-487-001A-11  
Sequence 11, Application US/08487001A  
Patent No. 5725862  
GENERAL INFORMATION:  
APPLICANT: FRANK, GLENN R.

APPLICANT: HUNTER, SHIRLEY WU  
APPLICANT: WALLENFELS, LYNDIA  
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA  
TITLE OF INVENTION: PROTEINS AND APPARATUS TO COLLECT SUCH PROTEINS  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SHERIDAN ROSS & MCINTOSH  
STREET: 1700 LINCOLN STREET, SUITE 3500  
CITY: DENVER  
STATE: COLORADO  
COUNTRY: U.S.A.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,001A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: 2618-17-C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-487-001A-11

Query Match 58.5%; Score 24; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 5 ELKVF 9  
DB 3 ELKVF 7

RESULT 9  
US-08-630-822A-11  
Sequence 11, Application US/08630822A  
Patent No. 5840695  
GENERAL INFORMATION:  
APPLICANT: FRANK, GLENN R.  
APPLICANT: HUNTER, SHIRLEY WU  
APPLICANT: WALLENFELS, LYNDIA  
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS  
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SHERIDAN ROSS P.C.  
STREET: 1700 LINCOLN STREET, SUITE 3500  
CITY: DENVER  
STATE: COLORADO  
COUNTRY: U.S.A.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,822A  
FILING DATE: 11-APR-1996  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: CONNELL, GARY J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-17-C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-630-822A-11

Query Match 58.5%; Score 24; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ELKRV 9  
DB 3 ELKRV 7

RESULT 10  
US-08-711-905-11  
Sequence 11, Application US/08711905  
Patent No. 5927230  
GENERAL INFORMATION:  
APPLICANT: FRANK, GLENN R.  
APPLICANT: WU HUNTER, SHIRLEY  
APPLICANT: WALLENFELDS, LYNDY  
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND  
TITLE OF INVENTION: APPARATUS TO COLLECT SUCH PROTEINS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SHERIDAN ROSS & MCINTOSH  
STREET: 1700 LINCOLN ST., SUITE 3500  
CITY: DENVER  
STATE: CO  
COUNTRY: USA  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/711,905  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: VERSER, CAROL TALKINGTON  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: 2618-17  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/863-9700  
TELEFAX: 303/863-0223  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE:  
US-08-711-905-11

Query Match 58.5%; Score 24; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ELKRV 9  
DB 3 ELKRV 7

DB 3 ELKRV 7

RESULT 11  
US-09-005-069-11  
Sequence 11, Application US/09005069  
Patent No. 593470  
GENERAL INFORMATION:  
APPLICANT: FRANK, GLENN R.  
APPLICANT: HUNTER, SHIRLEY WU  
APPLICANT: WALLENFELDS, LYNDY  
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS  
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross P.C.  
STREET: 1700 Lincoln Street, Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005,069  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/630,822  
FILING DATE: 11-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: CONNELL, GARY J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-17-C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-005-069-11

Query Match 58.5%; Score 24; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ELKRV 9  
DB 3 ELKRV 7

RESULT 12  
US-08-465-325-131  
Sequence 131, Application US/08465325  
Patent No. 5686563  
GENERAL INFORMATION:  
APPLICANT: Magalain Pharmaceuticals Inc.  
APPLICANT: 5110 Campus Drive  
APPLICANT: Plymouth Meeting, PA 19462  
TITLE OF INVENTION: Biologically Active Peptides Having  
TITLE OF INVENTION: N-Terminal Substitutions  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &  
Dunnet

STREET: 1300 I. Street, N.W. Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,325  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/184,462  
FILING DATE: 18-JAN-94  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/891,201  
FILING DATE: 01-JUN-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Fordis, Jean B  
REGISTRATION NUMBER: 32,984  
REFERENCE/DOCKET NUMBER: 05387.0021-03000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4400  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 131:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-465-325-131

Query Match 53.7%; Score 22; DB 1; Length 11;  
Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 2 LAKELK 7  
I I I I I  
Db 4 LKELK 9

RESULT 13  
US-09-115-737-131  
Sequence 131, Application US/09115737  
Patent No. 6348445  
GENERAL INFORMATION:  
APPLICANT: U. Prasad Karl  
Michael McLane  
Taify J. Williams  
TITLE OF INVENTION: Biologically Active Peptides with Reduced  
Toxicity in Animals and a Method for Preparing Same  
NUMBER OF SEQUENCES: 156  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
Dunne, L.L.P.  
STREET: 1300 I Street, N.W. Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.3  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/115,737  
FILING DATE: 15-Jul-1998

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/465,330  
FILING DATE: 05-JUN-1995  
APPLICATION NUMBER: 08/184,462  
FILING DATE: 18-JAN-94  
APPLICATION NUMBER: 07/891,201  
FILING DATE: 01-JUN-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Fordis, Jean B  
REGISTRATION NUMBER: 32,984  
REFERENCE/DOCKET NUMBER: 05387.0021-06000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4400  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 131:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 131:  
US-09-115-737-131

Query Match 53.7%; Score 22; DB 4; Length 11;  
Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 2 LAKELK 7  
I I I I I  
Db 4 LKELK 9

RESULT 14  
US-08-578-674-10  
Sequence 10, Application US/08578674  
Patent No. 6077827  
GENERAL INFORMATION:  
APPLICANT: Kolbe, Hanno V. J.  
APPLICANT: RASMUSSEN, Ulla B.  
APPLICANT: KREIL, Gundbert  
APPLICANT: ACHSTEITER, Tilman  
TITLE OF INVENTION: FAMILY OF PEPTIDES KNOWN AS XENOXINS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/578,674  
FILING DATE: 28-DEC-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 90 07901  
FILING DATE: 29-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 94 00202  
FILING DATE: 11-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 9400062.9  
FILING DATE: 11-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M.

Thu Aug 22 09:00:11 2002

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Page 7

REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 017753-071  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..12  
OTHER INFORMATION: /note="xenoxin-1, alkylated,  
US-08-578-674-10  
fragment C1(2)"

Query Match 53.7% Score 22: DB 3; Length 12;  
Best Local Similarity 71.4% Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 2 LAKTLKF 8  
DB 2 LAKTLKF 8

RESULT 15  
US-09-498-346-10  
Sequence 10, Application US/09498346  
Patent No. 6277822  
GENERAL INFORMATION:  
APPLICANT: KOLBE, Hanno V.J.  
APPLICANT: RASMUSSEN, Ulla B.  
APPLICANT: KREIL, Gunther  
APPLICANT: ACHSTER, Tilman  
TITLE OF INVENTION: FAMILY OF PEPTIDES KNOWN AS XENOXINS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/498,346  
FILING DATE: 04 FEB-2000  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER: US 08/578,674  
FILING DATE: 28-DEC-1995  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER: FR 90 07901  
FILING DATE: 29-JUN-1993  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER: FR 94 00202  
FILING DATE: 11-JAN-1994  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER: FR 9400062.9  
FILING DATE: 11-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Neuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 017753-071  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..12  
OTHER INFORMATION: /note="xenoxin-1, alkylated,  
US-09-498-346-10  
fragment C1(2)"

Query Match 53.7% Score 22: DB 4; Length 12;  
Best Local Similarity 71.4% Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0.  
OY 2 LAKTLKF 8  
DB 2 LAKTLKF 8

Search completed: August 21, 2002, 15:28:21  
Job time: 130 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 21, 2002, 15:28:27 ; Search time 10.24 Seconds  
(without alignments)

34.031 Million cell updates/sec

Title: US-09-633-364-6827

Sequence: 1 VLAKELKPV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 740

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	20	48.8	15	1	LCK_DROME
2	18	43.9	14	1	MAST_VESMA
3	17	41.5	10	1	SYK_CAMUP
4	17	41.5	13	1	CH60_CANPA
5	16	39.0	10	1	ESL_IACCA
6	16	39.0	13	1	BS19_ASHYP
7	16	39.0	14	1	MAST_VESLE
8	16	39.0	14	1	MAST_VESYA
9	16	39.0	15	1	ACPA_ACICA
10	15	36.6	13	1	CRBL_VESOR
11	15	36.6	14	1	COX2_THIOB
12	15	36.6	15	1	R13A_SPIOT
13	15	36.6	15	1	COX2_SHEEP
14	14	34.1	10	1	R10E_ACHLA
15	14	34.1	11	1	Q20A_COMTE
16	14	34.1	12	1	SO15_BACSU
17	14	34.1	13	1	CRBL_VESLE
18	14	34.1	13	1	NO40_PEA
19	14	34.1	15	1	MAST_PARD
20	14	34.1	15	1	EF1A_MICCK
21	14	34.1	9	1	FAR3_HIRME
22	13	31.7	10	1	FAR3_ASCSU
23	13	31.7	10	1	Q20B_COMTE
24	13	31.7	10	1	R20A_PIPNS
25	13	31.7	10	1	TKN1_SCYCA
26	13	31.7	10	1	TKU1_UREUN
27	13	31.7	13	1	CRBL_VESAN
28	13	31.7	13	1	CRBL_VESSTR
29	13	31.7	13	1	IDHC_PIG
30	13	31.7	13	1	PSAI_PEA
31	13	31.7	14	1	MAST_VESCR
32	13	31.7	14	1	UC15_MAIZE
33	13	31.7	14	1	UC15_MAIZE

34	12	29.3	4	1	FAR3_HIRME	P42562 hirudo medi
35	12	29.3	4	1	FLRF_HIRME	P42561 hirudo medi
36	12	29.3	7	1	CCPL_ENTFA	P20104 enterooccu
37	12	29.3	7	1	FAR1_HELTI	P41871 helisma tr
38	12	29.3	7	1	FAR1_PROCL	P38499 procambaru
39	12	29.3	7	1	FAR2_ASCSU	P31890 ascaris suu
40	12	29.3	7	1	FAR2_PROCL	P38498 procambaru
41	12	29.3	7	1	FWA3_ACHPU	P35921 achata fu
42	12	29.3	8	1	CND1_ENTFA	P13268 enterooccu
43	12	29.3	8	1	FAR1_PANRE	P41872 panagrelus
44	12	29.3	8	1	FAR3_HOMAN	P4186 homatus ame
45	12	29.3	8	1	FAR4_HOMAN	P4187 homatus ame

## ALIGNMENTS

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RESULT 1
LCK_DROME STANDARD: PRT: 15 AA.
AC P81829;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leucokinin (DLK).
GN pp OR DLK.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Phylotocidae; Drosophilidae; Drosophila.
OX NBL_rapid7227;
RN [1]
RP SEQUENCE.
RC TISSUE=Neurosecretory cell;
RX MEDLINE=20044845; PubMed=10574744;
RA Terhaz S., O'Connell F.C., Pollock V.P., Kean L., Davies S.A.,
RA Veenstra J.A., Dow J.A.T.;
RT "Isolation and characterization of a leucokinin-like peptide of
RT Drosophila melanogaster."
RT J. Exp. Biol. 202:3667-3676(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Celniker S.E., Agapayni A., Arcalata T.T., Baxter E., Blazek R.G.,
RA Buttenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomolan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Paclieb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Sylvestre R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RT -1- FUNCTION: ACTS THROUGH INTRACELLULAR CALCIUM IN MALPIGHIAN TUBULE
RT STELLATE CELLS TO RAISE CHLORIDE CONDUCTANCE.
CC -----
CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AC006496; -; NOT_ANNOTATED_CDS.
CC Flybase: FBgn0028418; Leucokinin.
CC Neuropeptide; Annotation.
CC MOD_RES 15;
CC SEQUENCE 15 AA; 1743 MW; 4793A08F51C9525 CRC64;
Query Match 48.8%; Score 20; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0.

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OY      1 VLAKELKF 8
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DB      4 VLCKKORF 11

RESULT 2
ID      MAST_VESMA STANDARD: PRT: 14 AA.
AC      P04205;
DT      20-MAR-1987 (Rel. 04, Created)
DT      20-MAR-1987 (Rel. 04, Last sequence update)
DT      01-AUG-1992 (Rel. 23, Last annotation update)
DE      Mastoparan M (Mast cell-degranulating peptide).
OS      Vespa mandarinia (Hornet).
OC      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC      Eukaryota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC      Vespoidea; Vespidae; Vespinae; Vespa.
OX      NCBI_TaxID=7446;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Venom;
RA      Hirai Y., Yasuhara T., Yoshida H., Nakajima T.;
RT      "A new mast cell degranulating peptide, mastoparan-M, in the venom of
RT      the hornet Vespa mandarinia";
RL      Biomed. Res. 2:447-449(1981).
CC      -1- FUNCTION: Mast cell DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
CC      PIR: A01777; CQVHNM.
DR      Mast cell degranulation; Venom; Amidation.
KW      MOD_RES 14.
FT      MOD_RES 14.
SQ      SEQUENCE 14 AA: 1480 MW: C85ATECAID7B0DD CRC64;

Query Match 43.9%; Score 18; DB 1; Length 14;
Best Local Similarity 80.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      2 LAKEL 6
        1 1 1 1
DB      9 LAKKL 13

RESULT 3
ID      SYK_CAMUP STANDARD: PRT: 10 AA.
AC      Q46464;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LYSRS)
DE      (Fragment).
OS      LYS.
GN      Campylobacter upsaliensis.
OC      Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC      Campylobacter.
OX      NCBI_TaxID=28080;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC 43954;
RA      MEDLINE=97149302; PubMed=8996110;
RA      Bourke B., Rashid S.T., Bingham H.L., Chan V.L.;
RT      "Characterization of Campylobacter upsaliensis for and its
RT      localization in a highly conserved region of the Campylobacter
RT      genome.";
RL      Gene 183:219-224(1996).
CC      -1- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) -> AMP + diphosphate
CC      + L-lysyl-tRNA(Lys).
CC      -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is not modified
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
CC      EMBL: L77076; ABA1342.1;
DR      Interpro; IPR002106; AA_TRNA_Ligase_11.
DR      PROSITE; PS00179; AA_TRNA_Ligase_11-1; PARTIAL.
DR      PROSITE; PS00339; AA_TRNA_Ligase_11-2; PARTIAL.
KW      Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT      NON_TER 1.
SQ      SEQUENCE 10 AA: 1218 MW: 9C6A46AB1372B05 CRC64;

Query Match 41.5%; Score 17; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

OY      2 LAKELK 7
        1 1 1 1
DB      1 LKSELK 6

RESULT 4
ID      CH60_CANFA STANDARD: PRT: 13 AA.
AC      P49818;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      60 kDa heat shock protein, mitochondrial (Hsp60) (60 kDa chaperonin)
DE      (Cpn60) (heat shock protein 60) (Hsp-60) (Mitochondrial matrix protein
DE      p17) (Fragment).
OS      HSP60.
GN      Canis familiaris (Dog).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX      NCBI_TaxID=9615;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Heart;
RA      Dunn M.J., Corbett J.M., Wheeler C.H.;
RT      "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT      dog heart proteins.";
RL      Electrophoresis 18:2795-2802(1997).
CC      -1- FUNCTION: IMPLICATED IN MITOCHONDRIAL PROTEIN IMPORT AND
CC      MACROMOLECULAR ASSEMBLY. MAY FACILITATE THE CORRECT FOLDING OF
CC      IMPORTED PROTEINS. MAY ALSO PREVENT MISFOLDING AND PROMOTE THE
CC      REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED
CC      UNDER STRESS CONDITIONS IN THE MITOCHONDRIAL MATRIX.
CC      -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC      -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR      HSC-2DPAGE; P49818; DOG.
DR      Interpro; IPR001844; Chaperonins_cpn60.
DR      PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.
KW      Chaperone; ATP-binding; Mitochondrion.
FT      NON_TER 13.
SQ      SEQUENCE 13 AA: 1383 MW: C6571E012DBFE879 CRC64;

Query Match 41.5%; Score 17; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0.

OY      3 AKELKF 8
        1 1 1 1
DB      1 AKDYKF 6

RESULT 5

```

[illegible]

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OY      1 VLAKELK 7
      1: 1:1
DB      2 VILKAIK 8

RESULT 7
MAST_VESLE STANDARD: PRT: 14 AA.
AC PO1514:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mastoparan.
VE Vesputia lewisii (yellow jacket) (Nesb).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vesputidae; Vesputinae; Vesputine; Vesputia.
OX NCBI_TaxID=1452;
RN (1)
RP SEQUENCE AND SYNTHESIS.
RC TISSUE=Venom.
RC MEDLINE=80155137; PubMed=540362;
RA "A new mast cell degranulating peptide 'mastoparan' in the venom of
RT Vesputia lewisii."
RT Chem. Pharm. Bull. 27:1942-1944(1979).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
CC THAT COUPLE TO PHOSPHOLIPASE C.
PIR: A01776; OMNAVY.
KW Mast cell degranulation; Venom; Amidation.
FT MOD_RES 14 14
SQ SEQUENCE 14 AA; 1480 MM; CC0CCEAID7B00DD CRC64;

Query Match 39.0%; Score 16; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1;ge+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      2 LAKEL 6
      1:1:1
DB      9 IAKKI 13

RESULT 8
MAST_VESXA STANDARD: PRT: 14 AA.
AC PO1515:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Mastoparan X (Hr-X) (Japanese hornet).
OS Vespa xanthoptera; Arthropoda; Tracheata; Hexapoda; Insecta;
OS Eukaryota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vesputidae; Vesputinae; Vesputine; Vespa.
OX NCBI_TaxID=7448;
RN (1)
RP SEQUENCE.
RC TISSUE=Venom;
RC MEDLINE=80155138; PubMed=540363;
RA Hirai Y., Kuwada M., Yasuhara T., Yoshida H., Nakajima T.;
RA "A new mast cell degranulating peptide homologous to mastoparan in
RT the venom of Japanese hornet (Vespa xanthoptera)."
RT Chem. Pharm. Bull. 27:1945-1946(1979).
RN (2)
RP STRUCTURE BY NMR.
RA MEDLINE=92304942; PubMed=1610813;
RA Wakamatsu K., Okada A., Miyazawa T., Ohya M., Higashijima T.;
RT "Membrane-bound conformation of mastoparan X, a G-protein activating
RT peptide."
RT Biochemistry 31:5654-5660(1992).
RN (3)

```

```

STRUCTURE BY NMR. PubMed-9537994;
MEDLINE-98206894;
Kusunoki H., Makamatsu K., Sato K., Miyazawa T., Kohno T.;
" G protein-bound conformation of mastoparan-X: heteronuclear
multidimensional transferred nuclear Overhauser effect analysis of
peptide uniformly enriched with 13C and 15N ";
Biochemistry 37:4782-4790(1998)
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
CC THAT COUPLE TO PHOSPHOLIPASE C.
DR PIR: A01778; QWVAXX.
DR PDB: 1A13; 16-FEB-99.
CC MOD.RES 14
CC MOD.RES 14
FT SEQUENCE 14 AA: 1557 MW: C85D0D7AA7AB0DD CRC64;

Query Match 39.0%; Score 16; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAKEL 6
DB 9 MAKKL 13

RESULT 9
ACBL_VESOR STANDARD; PRT; 15 AA.
AC 17236;
AC 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
D3 Isocitrate lyase (EC 4.1.3.1) (isocitrate) (ICU)
D3 (Fragment).
G4 ACBL.
G4 Acinetobacter calcoaceticus.
G4 Bacteroides proteobacteria; gamma subdivision; Moraxellaceae;
G4 Acinetobacter.
OK NCBI_TaxID-471;
RN [1]
RP SEQUENCE:
MEDLINE-92041568; PubMed-1938889;
RX Hoyt J.C., Johnson K.E., Reeves H.C.;
RT "Purification and characterization of Acinetobacter calcoaceticus
isocitrate lyase.";
RL J. Bacteriol. 173:6844-6848(1991).
CC -1- CATALYTIC ACTIVITY: isocitrate = succinate + glyoxylate.
CC -1- PATHWAY: FIRST STEP IN GLYOXYLATE BYPASS, AN ALTERNATIVE TO THE
CC TRICARBOXYLIC ACID CYCLE (IN BACTERIA, PLANTS, AND FUNGI).
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ISOCITRATE LYASE FAMILY.
DR PIR: A41338; A41338.
DR InterPro: IPR000918; Isocit_Lyase.
DR PROSITE: PS00161; ISOCITRATE LYASE; PARTIAL.
KM Glyoxylate bypass; Tricarboxylic acid cycle; Lyase.
FT MOD.RES 15
FT NON TER 15
FT SEQUENCE 15 AA: 1710 MW: 83AE726B1F2F96B3 CRC64;

Query Match 39.0%; Score 16; DB 1; Length 15;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 KELK 7
DB 11 RELK 14

RESULT 10
CRBL_VESXA STANDARD; PRT; 13 AA.
AC 17234;

STRUCTURE BY NMR. PubMed-9537994;
MEDLINE-98206894;
Kusunoki H., Makamatsu K., Sato K., Miyazawa T., Kohno T.;
" G protein-bound conformation of mastoparan-X: heteronuclear
multidimensional transferred nuclear Overhauser effect analysis of
peptide uniformly enriched with 13C and 15N ";
Biochemistry 37:4782-4790(1998)
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
CC OF NEUTROPHILS.
DR PIR: A01778; QWVAXX.
DR PDB: 1A13; 16-FEB-99.
CC MOD.RES 14
CC MOD.RES 13
FT SEQUENCE 13 AA: 1368 MW: C85040365D9233D CRC64;

Query Match 36.6%; Score 15; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLAKEL 6
DB 4 IIAKLL 9

RESULT 11
CRBL_VESOR STANDARD; PRT; 14 AA.
AC 17236;
AC 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last annotation update)
DE Histamine releasing peptide II (HR-II).
OS Vespa orientalis (oriental hornet).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vespidae; Vespinae; Vespa.
OK NCBI_TaxID-7447;
RN [1]
RP SEQUENCE:
RC TISSUE-Venom;
RA Miroshnikov A.I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,
RA Rozyanov B.V., Gushchin I.S.;
RT "Structure and properties of histamine releasing peptides from the
RT venom of Vespa orientalis hornet.";
RL Bioorg. Khim. 7:1467-1477(1981).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
CC OF NEUTROPHILS.
CC PIR: JN0390; JN0390.
DR Mast cell degranulation; Chemotaxis; Venom; Amidation.
KM MOD.RES 14
KM MOD.RES 14
FT SEQUENCE 14 AA: 1524 MW: 22015B4A6CEDFD38 CRC64;

Query Match 36.6%; Score 15; DB 1; Length 14;
Best Local Similarity 42.9%; Pred. No. 3.1e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 VLAKEL 7
DB 5 ILGKLV 11

RESULT 12
COXI_THUOB STANDARD; PRT; 15 AA.
ID COXI_THUOB

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P80978;  
 01-NOV-1997 (Rel. 35, Created)  
 01-NOV-1997 (Rel. 35, Last sequence update)  
 01-NOV-1997 (Rel. 35, Last annotation update)  
 Cytochrome c oxidase polypeptide VIC-2 (EC 1.9.3.1) (Fragments).  
 Rhynchosus obsesus (Bigeye tuna).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;  
 Scombridae; Thunnus.  
 NCBI\_TaxID=8241;  
 [1]  
 SEQUENCE  
 TISSUE=heart;  
 MEDLINE=97454291; PubMed=9310366;  
 Arnold S., Lee I., Kim K., Song E., Linder D., Lottspeich F.,  
 Kadembach B.,  
 "The subunit structure of cytochrome c oxidase from tuna heart and  
 liver.",  
 Eur. J. Biochem. 248:99-103(1997).  
 -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 MITOCHONDRIAL ELECTRON TRANSPORT.  
 -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome  
 c + 2 H(2)O.  
 -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 Oxidoreductase; Inner membrane; Mitochondrion.  
 NON\_TER 1 1  
 FT NON\_CONS 8 9  
 FT NON\_TER 15 15  
 SO SEQUENCE 15 AA; 1696 MW; 4CAC966C73A40294 CRC64;

Query Match 36.6%; Score 15; DB 1; Length 15;  
 Best Local Similarity 60.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLAK 5  
 : 1 1  
 Db 5 VVAK 9

RESULT 13  
 R13A\_SPTOL STANDARD: PRT; 15 AA.  
 AC P82454;  
 DT 01-MAR-2002 (Rel. 41, Created)  
 DT 01-MAR-2002 (Rel. 41, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE 60S ribosomal protein L13a (Fragment).  
 GN RPL13A.  
 OS Spinacia oleracea (Spinach).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 CC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.  
 NCBI\_TaxID=3562;  
 OX [1]  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=CV. ALVARO; TISSUE=Leaf;  
 RA Yamaguchi K., Subramanian A.R.;  
 RT "N-terminal sequence of spinach cytosolic 60S ribosomal protein  
 L13a".  
 RT Submitted (APR-2000) to the SWISS-PROT data bank.  
 CC -!- SIMILARITY: BELONGS TO THE L13P FAMILY OF RIBOSOMAL PROTEINS.  
 DR InterPro: IPR001074; RIBOSOMAL\_L13.  
 DR PROSITE: PS00783; RIBOSOMAL\_L13; PARTIAL.  
 KM RIBOSOMAL PROTEIN.  
 FT NON\_TER 15  
 FT SEQUENCE 15 AA; 1489 MW; C7B9C80F5A039EB3 CRC64;

Query Match 36.6%; Score 15; DB 1; Length 15;  
 Best Local Similarity 33.3%; Pred. No. 3.4e+03;

Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 VLAK 6  
 : 1 1  
 Db 6 IMARKV 11

RESULT 14  
 COXO\_SHEEP STANDARD: PRT; 10 AA.  
 AC P80337;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)  
 (Fragment).  
 DE (Fragment).  
 OS Ovis aries (Sheep).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 OX [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart, and Liver;  
 RA Freund R., Kadembach B.;  
 RL Submitted (MAR-1994) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome  
 c + 2 H(2)O.  
 Oxidoreductase; Mitochondrion.  
 NON\_TER 10  
 FT NON\_TER 10  
 SO SEQUENCE 10 AA; 1027 MW; C4E95CA33DC7633D CRC64;

Query Match 34.1%; Score 14; DB 1; Length 10;  
 Best Local Similarity 42.9%; Pred. No. 3.7e+03;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 VLAKEL 7  
 : 1 1  
 Db 1 ITAKPAK 7

RESULT 15  
 RL16\_ACHLA STANDARD: PRT; 10 AA.  
 ID RL16\_ACHLA  
 AC P29221;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE 50S ribosomal protein L16 (Fragment).  
 GN RPLP.  
 OS Acholeplasma laidlawi.  
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;  
 CC Acholeplasmataceae; Acholeplasma.  
 OX NCBI\_TaxID=2148;  
 OX [1]  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=92210505; PubMed=1556079;  
 RA Lim P.O., Sears B.B.;  
 RT "Evolutionary relationships of a plant-pathogenic mycoplasma like  
 organism and Acholeplasma laidlawi deduced from two ribosomal protein  
 gene sequences.";  
 RT J. Bacteriol. 174:2606-2611(1992).  
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS  
 LOCATED AT THE A SITE OF THE PEPTIDYLTRANSFERASE CENTER  
 (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE L16P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

-----  
CC EMBL; M74771; AAA21914.1; .  
DR PIR; F41839; F41839.  
DR InterPro; IPR000114; Ribosomal\_L16.  
DR PROSITE; PS00586; RIBOSOMAL\_L16\_1; PARTIAL.  
DR PROSITE; PS00701; RIBOSOMAL\_L16\_2; PARTIAL.  
KW Ribosomal protein; rRNA-binding.  
FT NON\_TER 10 10  
SO SEQUENCE 10 AA; 1324 MW; B386A21B4032766 CRC64;

Query Match 34.1%; Score 14; DB 1; Length 10;  
Best Local Similarity 25.0%; Pred. No. 3.7e+03;  
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 VLAKELKF 8  
Db 2 LMPKRTKY 9

Search completed: August 21, 2002, 15:31:51  
Job time: 204 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: August 21, 2002, 15:27:11 ; Search time 14.12 seconds  
(without alignments)  
61.247 Million cell updates/sec

Title: US-09-633-364-6827  
Perfect score: 41  
Sequence: 1 VLAKELKFV 9

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 28338 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 2519

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: 1: PIR\_71:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	58.5	11	2	PC2372
2	20	48.6	15	2	B41436
3	19	46.3	10	2	A44871
4	19	46.3	14	2	S72217
5	18	43.9	13	2	S28425
6	18	43.9	14	1	OMVHMM
7	18	43.9	14	2	PC2373
8	17	41.5	14	2	PN0147
9	17	41.5	15	2	PA0053
10	16.5	40.2	12	2	S01222
11	16	39.0	7	2	PS0754
12	16	39.0	10	2	S48182
13	16	39.0	12	2	C36201
14	16	39.0	12	2	S47360
15	16	39.0	14	1	OMVHMM
16	16	39.0	14	1	OMVHMM
17	16	39.0	14	1	OMVHMM
18	16	39.0	14	2	PN0151
19	16	39.0	15	2	PN0117
20	16	39.0	15	2	A41338
21	16	39.0	15	2	S36890
22	15	36.6	10	2	S06964
23	15	36.6	10	2	S38304
24	15	36.6	11	2	S33519
25	15	36.6	12	2	A58501
26	15	36.6	13	2	A61288
27	15	36.6	14	2	JN0390
28	15	36.6	14	2	S29789
29	15	36.6	15	2	PA0097

30	15	36.6	15	2	I50503	agrin - electric r
31	15	36.6	15	2	S7987	cytochrome-c oxida
32	14	34.1	9	2	G58502	kidney and bladder
33	14	34.1	9	2	I54379	gene NF2 protein -
34	14	34.1	9	2	B30572	T-cell receptor be
35	14	34.1	10	2	F41839	ribosomal protein
36	14	34.1	10	2	PH0113	alpha-amylase (EC
37	14	34.1	10	2	C10572	T-cell receptor be
38	14	34.1	11	2	S66606	guinoline 2-oxidor
39	14	34.1	11	2	B19853	luciferase - pro
40	14	34.1	11	2	C59151	protein-tyrosine k
41	14	34.1	11	2	H84082	hypothetical prote
42	14	34.1	12	2	S15815	translation elonga
43	14	34.1	12	2	G48215	urease (EC 3.5.1.5
44	14	34.1	12	2	S68402	NAD(+)-glycohydrol
45	14	34.1	12	2	PH1466	T-cell receptor de

## ALIGNMENTS

RESULT 1  
PC2372  
58K heat shock protein:groEL [similarity] - Bacillus cereus (strain ts-4) (fragment)  
C:Species: Bacillus cereus  
C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: PC2372  
R:Matsumoto, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S  
Biosci. Biotechnol. Biochem. 59, 231-235, 1995  
A>Title: Identification of DNA-binding proteins changed after induction of sporula  
A:Reference number: PC2369; MUID:95218265  
A:Accession: PC2372  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <MS>  
C:Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 58.5% Score 24; DB 2; Length 11;  
Best Local Similarity 66.7% Pred. No. 67;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AKELKF 8  
DB 1 AKDIKF 6  
RESULT 2  
B41436  
ovostatin - green sea turtle (fragment)  
C:Species: Chelonia mydas (green sea turtle)  
C>Date: 21-Apr-1992 #sequence\_revision 21-Apr-1992 #text\_change 18-Jun-1993  
C:Accession: B41436  
R:Osada, T.; Sasaki, T.; Imai, A.  
J. Biochem. 103, 212-217, 1988  
A>Title: Purification and characterization of alpha-macroglobulin and ovomacroglob  
A:Reference number: A41436; MUID:88227890  
A:Accession: B41436  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <OS>

Query Match 48.8% Score 20; DB 2; Length 15;  
Best Local Similarity 57.1% Pred. No. 68+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AKELKFV 9  
DB 2 APELOLV 8  
RESULT 3

A44871  
monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - soybean (fragment)  
C:Species: Glycine max (soybean)  
C:Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 12-Sep-1997  
C:Accession: A44871  
R:Belton, D.A.; Langeberg, L.; Robbins, M.  
R:Biochem. Biophys. 297, 281-286, 1992  
A:Title: Purification and characterization of monodehydroascorbate reductase from soybean  
A:Reference number: A44871; MUID:92088257  
A:Accession: A44871  
A:Status: Preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <DAL>  
A:Experimental source: root nodules, cv. Williams  
A:Note: sequence extracted from NCBI backbone (NCBIP:71052)  
C:Keywords: oxidoreductase

Query Match 46.3%; Score 19; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 7.3e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 AKELFV 9  
11111  
Db 1 AKTKYI 7

RESULT 4  
S72217  
D:arabinose 1-dehydrogenase (NAD(P)+) (EC 1.1.1.117) - yeast (Candida albicans) (fragment)  
C:Species: Candida albicans  
C:Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 13-Mar-1998  
C:Accession: S72217  
R:Kim, S.T.; Huh, W.K.; Kim, J.Y.; Hwang, S.W.; Kang, S.O.  
R:Biochim. Biophys. Acta 1297, 1-8, 1996  
A:Title: D-Arabinose dehydrogenase and biosynthesis of erythroascorbic acid in Candida  
A:Reference number: S72217; MUID:96439039  
A:Accession: S72217  
A:Molecule type: protein  
A:Residues: 1-14 <KIM>  
C:Keywords: oxidoreductase

Query Match 46.3%; Score 19; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 LAELKF 8  
11111  
Db 3 LAELDF 9

RESULT 5  
S28423  
Z0K protein - rape (fragment)  
C:Species: Brassica napus (rape)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Jan-1995  
C:Accession: S28423  
R:Hellner, A.; Leadlay, P.F.; Slabas, A.R.  
R:Plant Mol. Biol. 20, 763-780, 1992  
A:Title: Induction, purification and characterisation of acyl-ACP thioesterase from develope  
A:Reference number: S28424; MUID:93099229  
A:Accession: S28425  
A:Status: Preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <HEL>

Query Match 43.9%; Score 18; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLAKEL 6

Db 7 ITAKEL 12  
11111

RESULT 6  
OMVHM  
Mastoparan M - hornet (Vespa mandarinia)  
N:Alternate names: mast cell degranulating peptide  
C:Species: Vespa mandarinia  
C:Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 08-Dec-1995  
C:Accession: A01777  
R:Hirai, Y.; Yasuhara, T.; Yoshida, H.; Nakajima, T.  
R:Blomed. Res. 2, 447-449, 1981  
A:Title: A new mast cell degranulating peptide, mastoparan-M, in the venom of the }  
A:Reference number: A01777  
A:Accession: A01777  
A:Molecule type: protein  
A:Residues: 1-14 <HIR>  
C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation  
C:Superfamily: mastoparan  
C:Keywords: amidated carboxyl end; venom  
F:14/Modified site: amidated carboxyl end (Ileu) #status experimental

Query Match 43.9%; Score 18; DB 1; Length 14;  
Best Local Similarity 80.0%; Pred. No. 1.7e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAEL 6  
11111  
Db 9 LAELK 13

RESULT 7  
PC2373  
Probable IMP dehydrogenase (EC 1.1.1.205) [similarity] - Bacillus cereus (strain ts  
C:Species: Bacillus cereus  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 02-Sep-2000  
C:Accession: PC2373  
R:Matsumoto, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatanoto, S.  
R:Biochem. Biophys. Res. Commun. 231, 231-235, 1995  
A:Title: Identification of DNA-binding proteins changed after induction of sporulat  
A:Reference number: PC2369; MUID:95218265  
A:Accession: PC2373  
A:Status: Preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <MAS>  
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal hc  
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis

Query Match 43.9%; Score 18; DB 2; Length 14;  
Best Local Similarity 80.0%; Pred. No. 1.7e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 ELKRV 9  
11111  
Db 3 ESKRV 7

RESULT 8  
PN0147  
Omega-glutamine 1 and 2 - Aegilops longissima (fragment)  
C:Species: Aegilops longissima  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PN0147; PN0146  
R:Odintsova, T.I.; Egorov, T.A.  
R:Biokhimiia 55, 509-516, 1990  
A:Title: N-terminal sequences of omega-glutamins of Aegilops longissima: On the ori  
A:Reference number: PN0146; MUID:90283493  
A:Accession: PN0147  
A:Molecule type: protein  
A:Residues: 1-14 <ODI>

A: Experimental source: strain K-202  
A: Note: omega-gliadine 2 (amino-terminal fragment)  
A: Accession: P00146  
A: Molecule type: protein  
A: Residues: 1-9 <CD2>  
A: Experimental source: strain K-202  
A: Note: omega-gliadine 1 (amino-terminal fragment)

Query Match 41.5%: Score 17; DB 2; Length 14;  
Best Local Similarity 50.0%: Pred. No. 2.8e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 LAKEKF 7  
DB 7 ICKELQ 12

RESULT 9  
PA0053  
protein QP200006 - fungus (Fusarium sporotrichoides) (fragment)  
C: Species: Fusarium sporotrichoides  
C: Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
C: Accession: PA0053  
R: Chow, L.P.; Fukaya, N.; Sugita, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
Submitted to JIPID, October 1994  
A: Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich  
A: Reference number: PA0051  
A: Accession: PA0053  
A: Molecule type: protein  
A: Residues: 1-15 <CHO>

Query Match 41.5%: Score 17; DB 2; Length 15;  
Best Local Similarity 42.9%: Pred. No. 3e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 AKELKFV 9  
DB 2 AKELKPI 8

RESULT 10  
S01222  
translation elongation factor EF-Tu - Pseudomonas aeruginosa (fragment)  
C: Species: Pseudomonas aeruginosa  
C: Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 26-Aug-1999  
C: Accession: S01222  
R: Hughes, M.A.; Jones, D.S.  
Nucleic Acids Res. 16, 7193, 1988  
A: Title: A fragment of the Pseudomonas aeruginosa genome contains five rRNA genes, four  
A: Reference number: S01222; MUID: 88303352  
A: Accession: S01222  
A: Status: translation not shown  
A: Molecule type: DNA  
A: Residues: 1-12 <HUG>  
A: Cross-references: EMBL: X07950; NID: 945426; PIDN: CAA30775.1; PID: 945427  
C: Geneticks:  
A: Gene: tuftB  
C: Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog  
C: Keywords: GTP binding; protein biosynthesis

Query Match 40.2%: Score 16.5; DB 2; Length 12;  
Best Local Similarity 71.4%: Pred. No. 3e+03; 0; Indels 1; Gaps 1;  
Matches 5; Conservative 1; Mismatches 0;

OY 2 LAKEKLF 8  
DB 1 MAKE-KF 6

RESULT 11

PS0254  
18K protein 5507 - rice (strain Nihonbare) (fragment)  
C: Species: Oryza sativa (rice)  
C: Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Mar-1995  
C: Accession: PS0254  
R: Accetta, A.  
Submitted to JIPID, April 1993  
A: Reference number: PS0206  
A: Accession: PS0254  
A: Molecule type: protein  
A: Residues: 1-7 <TSU>  
A: Experimental source: leaf, chloroplast, strain Nihonbare  
A: Note: molecular weight 18K, pI 4.4

Query Match 39.0%: Score 16; DB 2; Length 7;  
Best Local Similarity 75.0%: Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAKE 5  
DB 3 LAKE 6

RESULT 12  
S48182  
bacterioferritin - Rhodobacter capsulatus  
C: Species: Rhodobacter capsulatus  
C: Date: 15-Jul-1995 #sequence\_revision 19-Oct-1995 #text\_change 07-May-1999  
C: Accession: S48182  
R: Ringeling, P.L.; Davy, S.L.; Monkara, F.A.; Hunt, C.; Dickson, D.P.E.; McEwen, J.  
Eur. J. Biochem. 223, 847-855, 1994  
A: Title: Iron metabolism in Rhodobacter capsulatus. Characterisation of bacterioferr  
A: Reference number: S48182; MUID: 94333369  
A: Accession: S48182  
A: Status: preliminary  
A: Molecule type: protein  
A: Residues: 1-10 <KIN>

Query Match 39.0%: Score 16; DB 2; Length 10;  
Best Local Similarity 50.0%: Pred. No. 3.2e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 AKELKF 8  
DB 5 AKYIEF 10

RESULT 13  
C36201  
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - apple tree (fragment)  
C: Species: Malus domestica (apple tree)  
C: Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 04-Feb-2000  
C: Accession: C36201; C33103  
R: Yip, W.K.; Dong, J.G.; Kenny, J.W.; Thompson, G.A.; Yang, S.F.  
Proc. Natl. Acad. Sci. U.S.A. 87, 7930-7934, 1990  
A: Title: Characterization and sequencing of the active site of 1-aminocyclopropane  
A: Reference number: A36201; MUID: 91045911  
A: Accession: C36201  
A: Molecule type: protein  
A: Residues: 1-12 <YIP>  
A: Experimental source: strain Golden delicious  
C: Superfamily: 1-aminocyclopropane-1-carboxylate synthase  
C: Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal  
F4/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 39.0%: Score 16; DB 2; Length 12;  
Best Local Similarity 60.0%: Pred. No. 3.9e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAKE 6



```

ESL_LACCA
ID ESL_LACCA STANDARD: PRT: 10 AA.
AC P81758:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Putative esterase/lipase (EC 3.1.-.-) (fragment).
OS Lactobacillus casei.
OC Lactobacillus.
OC Bacteriota; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1582;
RN [1]
RP SEQUENCE.
RC STRAIN=TFP731;
RA Lopez de Felipe F.;
RL Submitted (MAR-1999) to the SWISS-PROT data bank.
KM Hydrolyase; Serine esterase.
FT NON_TER 10
SQ SEQUENCE 10 AA: 1070 MW: 106132D732CAB1A0 CRC64;

Query Match 39.0%; Score 16; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLAKK 5
DB 6 VLAKK 10

RESULT 6
RS19_ASHYP STANDARD: PRT: 13 AA.
ID RS19_ASHYP
AC 044592:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 30S Ribosomal protein S19 (fragment).
GN RPS19 OR RPS19.
OS Ash yellow's phytoplasm.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Annelaplasmataceae; Phytoplasmata.
OX NCBI_TaxID=35780;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmata): a basis for
RT their classification."
RL J. Bacteriol. 176:5244-5254(1994).
CC -1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
DR EMBL: L26999; AA893936.1;
DR InterPro: IPR002222; RIBOSOMAL_S19.
DR PROSITE: PS00133; RIBOSOMAL_S19; PARTIAL.
KM Ribosomal protein, rRNA-binding.
FT NON_TER 1
SQ SEQUENCE 13 AA: 1433 MW: CECAD10B84E5305D CRC64;

Thu Aug 22 09:00:13 2002
00 0%: Score 16; DB 1; Length 13;
00 1.8e+03; Indels 0; Gaps 0;

OY 1 VLAKK 7
DB 2 VLAKK 8

RESULT 7
MAST_VESLE STANDARD: PRT: 14 AA.
ID MAST_VESLE
AC P01514:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JUN-1999 (Rel. 29, Last annotation update)
DE Mastoparan.
OS Vesputa lewisii (Yellow Jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vesputidae; Vespidae; Vespinae; Vesputa.
OX NCBI_TaxID=7452;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Venom;
RA MEDLINE=80155337; PubMed=540362;
RA Hirai Y., Yasuhara T., Yoshida H., Nakajima T., Fujino M., Kitada C.;
RT "A new mast cell degranulating peptide 'mastoparan' in the venom of
RT Vesputa lewisii."
RL Chem. Pharm. Bull. 27:1942-1944(1979).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
CC THAT COUPLE TO PHOSPHOLIPASE C.
DR PIR: A01776; OMWAVV.
KM Mast cell degranulation; Venom; Amidation.
FT MOD_RES 14
SQ SEQUENCE 14 AA: 1480 MW: CC0CECA1D7B00DD CRC64;

Query Match 39.0%; Score 16; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAKKI 6
DB 9 LAKKI 13

RESULT 8
MAST_VESXA STANDARD: PRT: 14 AA.
ID MAST_VESXA
AC P01515:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Mastoparan X (MP-X).
OS Vespa xanthoptera (Japanese hornet).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vespidae; Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7448;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA MEDLINE=80155338; PubMed=540363;
RA Hirai Y., Kuwada M., Yasuhara T., Yoshida H., Nakajima T.;
RT "A new mast cell degranulating peptide homologous to mastoparan in
RT the venom of Japanese hornet (Vespa xanthoptera)."
RL Chem. Pharm. Bull. 27:1945-1946(1979).
RN [2]
RP STRUCTURE BY NMR.
RA MEDLINE=92304942; PubMed=1610813;
RA Wakamatsu K., Okada A., Miyazawa T., Ohya M., Higashijima T.;
RT "Membrane-bound conformation of mastoparan X, a G-protein-activating
RT peptide."
RL Biochemistry 31:5654-5660(1992).
RN [3]

```

Db 2 LSKOL 6

RESULT 14  
S47360  
T-cell antigen receptor VJ junction beta chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
C:Accession: S47360  
R:Lehner, P.J.  
submitted to the EMBL Data Library, August 1994  
A:Description: Human HLA-A0201 restricted recognition of Influenza A is dominated by T  
A:Reference number: S47355  
A:Accession: S47360  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-12 <LEH>  
A:Cross-references: EMBL:Z35684; NID:9527457; PID:CA84753.1; PID:9527458  
C:Keywords: T-cell receptor

Query Match 39.0%; Score 16; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 AKEL 6  
|||  
Db 6 AKEL 9

RESULT 15  
OMNAVY  
mastoparan - yellowjacket (Vespula lewisii)  
C:Species: Vespula lewisii  
C:Date: 24-Sep-1981 #sequence\_revision 24-Sep-1981 #text\_change 08-Dec-1995  
C:Accession: A01776  
R:Hirai, Y.; Yasuhara, T.; Yoshida, H.; Nakajima, T.; Fujino, M.; Kitada, C.  
Chem. Pharm. Bull. 27, 1942-1944, 1979  
A:title: A new mast cell degranulating peptide mastoparan in the venom of Vespula-lewisii  
A:Reference number: A01776; MUID:80155337  
A:Accession: A01776  
A:Molecule type: protein  
A:Residues: 1-14 <HIR>  
A:Note: The active peptide was also synthesized  
C:Comment: This cytoactive peptide from wasp venom induces mast cell degranulation. The  
C:Superfamily: mastoparan  
C:Keywords: amidated carboxyl end  
F:14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 39.0%; Score 16; DB 1; Length 14;  
Best Local Similarity 60.0%; Pred. No. 4.6e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAKEL 6  
|||  
Db 9 LAKKI 13

Search completed: August 21, 2002, 15:30:29  
Job time: 198 sec



DE SHORTER ISOFORM OF INTERLEUKIN 15 (FRAGMENT).  
 GN IL15 OR INTERLEUKIN 15.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALBC;  
 RA Nishimura H.;  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALBC;  
 RA MEDLINE=98211658; PubMed=9551932;  
 RX Nishimura H., Mashizu J., Nakamura N., Enomoto A., Yoshikai Y.;  
 RT "Translational efficiency is up-regulated by alternative exon in  
 RT murine IL-15 mRNA.";  
 RL J. Immunol. 160:936-942(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Prinz M., Hantsch U.K., Kettenmann H., Kirchhoff F.;  
 RT "Alternative splicing of mouse IL-15 is due to the use of an internal  
 RT splice site in exon 5.";  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: A802307; BAA37122.1;  
 DR EMBL: AJ012587; CAA10069.1;  
 DR MGI: 103014; 1115  
 FT NON\_TER 14  
 SQ SEQUENCE 14 AA; 1503 MW; 62A3C3889924E2B CRC64;

Query Match 56.1%; Score 23; DB 11; Length 14;  
 Best Local Similarity 71.4%; Pred. No. 4.4e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 AKELKV 9  
 :|||  
 Db 5 SKELGV 11

RESULT 3  
 09S926 PRELIMINARY; PRT; 10 AA.  
 AC 09S926;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE MONODEHYDROSCORABATE REDUCTASE II, Mrit.  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 ON NCBI\_TaxID=3847;  
 RX [1]  
 RP SEQUENCE  
 RC MEDLINE=92088257; PubMed=1727643;  
 RA Dalton D.A., Langenberg L., Robbins M.;  
 RT Purification and characterization of monodehydroascorbate reductase  
 RT from soybean root nodules.  
 RL Arch. Biochem. Biophys. 292:281-286(1992)  
 SQ SEQUENCE 10 AA; 1153 MW; 848055045359D1 CRC64;

Query Match 46.3%; Score 19; DB 10; Length 10;  
 Best Local Similarity 42.9%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 AKELKV 9  
 :|||  
 Db 1 AKFKYI 7

RESULT 4  
 09QZD0 PRELIMINARY; PRT; 12 AA.  
 AC 09QZD0;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE SH2-CONTAINING INOSITOL PHOSPHATASE SHIP (FRAGMENT).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Tu Z., Ninos J., Wang J.W., Lemos M., Kerr M.;  
 RT "An embryonic SHIP isoform, generated by transcriptional initiation at  
 RT an internal site, participates in a different signaling complex than  
 RT its hematopoietic counterpart.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF189743; AAF08279.1;  
 FT NON\_TER 1  
 FT NON\_TER 12  
 SQ SEQUENCE 12 AA; 1372 MW; 42F1800FB43B727 CRC64;

Query Match 46.3%; Score 19; DB 11; Length 12;  
 Best Local Similarity 66.7%; Pred. No. 2.7e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLAKEL 6  
 :|||  
 Db 5 LLCKEL 10

RESULT 5  
 09L4M9 PRELIMINARY; PRT; 12 AA.  
 AC 09L4M9;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE GUANOSINE BIPHOSPHATE SYNTHETASE, PUTATIVE (FRAGMENT).  
 GN REL.  
 OS Streptococcus equisimilis  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
 OC Streptococcus.  
 ON NCBI\_TaxID=119602;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H46A;  
 RC MEDLINE=20123454; PubMed=10660058;  
 RA Geyer A., Schmidt K.H.;  
 RT "Genetic organisation of the M protein region in human isolates of  
 RT group C and G streptococci: two types of multigene regulator-like  
 RT (mgfC) regions.";  
 RL Mol. Gen. Genet. 262:965-974(2000).  
 DR EMBL: AJ133440; CAB70616.1;  
 FT NON\_TER 12  
 FT NON\_TER 12  
 SQ SEQUENCE 12 AA; 1334 MW; 0A82EC4258A72440 CRC64;

Query Match 43.9%; Score 18; DB 2; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 4.5e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAKEL 6  
 :|||  
 Db 1 MAKEL 5

RESULT 6  
 069232 PRELIMINARY; PRT; 12 AA.  
 ID 069232

AC 069232; PRELIMINARY; PRT: 12 AA.  
 DT 01-NOV-1996 (TREMBLER, 01, Created)  
 DT 01-NOV-1996 (TREMBLER, 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLER, 19, Last annotation update)  
 DE HERPESVIRUS SAIMIRI GENE 7 HOMOLOGUE (FRAGMENT).  
 OS Bovine herpesvirus 4.  
 OC Viruses; dsDNA viruses, no RNA stage: Herpesviridae;  
 OC Gammaherpesvirinae.  
 NCBI\_TaxID=10385;  
 RN NCBI\_TaxID=10385;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-V, TEST;  
 RX MEDLINE=93391082; PubMed=1355698;  
 RA Rublot M., Lomonte P., Leguare A.-S., Albrecht J.-C., Nicholas J.,  
 RA Fleckenstein B., Pastoret P.-P., Thiry E.,  
 RT "Genetic relationships between bovine herpesvirus 4 and the  
 RT gammaherpesviruses Epstein-Barr virus and herpesvirus saimiri."  
 RL Virology 190:654-665(1992).  
 DR EMBL: M90772; AAA46019.1; -;  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA: 1338 MW: 48800FF17ACDDDD7 CRC64;

Query Match 43.9%; Score 18; DB 12; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 4.5e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 OY 2 LAKELEY 9  
 DB 1 MARLEAV 8  
 ID 032704 PRELIMINARY; PRT: 11 AA.  
 AC 032704;  
 DT 01-NOV-1996 (TREMBLER, 01, Created)  
 DT 01-NOV-1996 (TREMBLER, 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLER, 19, Last annotation update)  
 DE NDHE PROTEIN (FRAGMENT).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.  
 NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRIGHT YELLOW 4; TISSUE=LEAF;  
 RX MEDLINE=88210537; PubMed=3329576;  
 RA Hayashida N., Matsubayashi T., Shinzaki K., Sugisura M., Inoue K.,  
 RA Hayama T.,  
 RT "The gene for the 9kd polypeptide, a possible apoprotein for the iron-  
 RT sulfur centers A and B of the photosystem I complex in tobacco  
 RT chloroplastDNA."  
 RL Curr. Genet. 12:247-250(1987).  
 DR EMBL: X05881; CAA29303.1; -;  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA: 1338 MW: 008165FE304776CB CRC64;

Query Match 41.5%; Score 17; DB 8; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 6 LKFV 9  
 DB 7 IKFV 10  
 ID 032704 PRELIMINARY; PRT: 11 AA.  
 AC 032704;  
 DT 01-NOV-1996 (TREMBLER, 01, Created)  
 DT 01-NOV-1996 (TREMBLER, 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLER, 19, Last annotation update)  
 DE NDHE PROTEIN (FRAGMENT).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.  
 NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRIGHT YELLOW 4; TISSUE=LEAF;  
 RX MEDLINE=88210537; PubMed=3329576;  
 RA Hayashida N., Matsubayashi T., Shinzaki K., Sugisura M., Inoue K.,  
 RA Hayama T.,  
 RT "The gene for the 9kd polypeptide, a possible apoprotein for the iron-  
 RT sulfur centers A and B of the photosystem I complex in tobacco  
 RT chloroplastDNA."  
 RL Curr. Genet. 12:247-250(1987).  
 DR EMBL: X05881; CAA29303.1; -;  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA: 1338 MW: 008165FE304776CB CRC64;

Query Match 41.5%; Score 17; DB 8; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 6 LKFV 9  
 DB 7 IKFV 10  
 ID 032704 PRELIMINARY; PRT: 11 AA.  
 AC 032704;  
 DT 01-NOV-1996 (TREMBLER, 01, Created)  
 DT 01-NOV-1996 (TREMBLER, 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLER, 19, Last annotation update)  
 DE NDHE PROTEIN (FRAGMENT).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.  
 NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRIGHT YELLOW 4; TISSUE=LEAF;  
 RX MEDLINE=88210537; PubMed=3329576;  
 RA Hayashida N., Matsubayashi T., Shinzaki K., Sugisura M., Inoue K.,  
 RA Hayama T.,  
 RT "The gene for the 9kd polypeptide, a possible apoprotein for the iron-  
 RT sulfur centers A and B of the photosystem I complex in tobacco  
 RT chloroplastDNA."  
 RL Curr. Genet. 12:247-250(1987).  
 DR EMBL: X05881; CAA29303.1; -;  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA: 1338 MW: 008165FE304776CB CRC64;

ID 090NV5 PRELIMINARY; PRT: 12 AA.  
 AC 090NV5;  
 DT 01-MAY-2000 (TREMBLER, 13, Created)  
 DT 01-MAY-2000 (TREMBLER, 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBLER, 19, Last annotation update)  
 DE INOSINE MONOPHOSPHATASE 2 (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97463449; PubMed=9322233;  
 RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,  
 RA Detera-Wadleigh S.D.,  
 RT "A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a  
 RT susceptibility region for bipolar disorder."  
 RL Mol. Psychiatry 2:393-397(1997).  
 DR EMBL: AF085629; AAD22139.1; JOINED.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 12 AA: 1408 MW: D29A162A15172B06 CRC64;

Query Match 41.5%; Score 17; DB 4; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 7.3e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 OY 4 KELEF 8  
 DB 5 KELEF 9  
 ID 090QF8 PRELIMINARY; PRT: 12 AA.  
 AC 090QF8;  
 DT 01-MAY-2000 (TREMBLER, 13, Created)  
 DT 01-MAY-2000 (TREMBLER, 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLER, 13, Last annotation update)  
 DE CAFFEYL-COA O-METHYLTRANSFERASE (FRAGMENT).  
 OS Coffea arabica (Coffea arabica).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferales; Pinaceae; Pinus.  
 NCBI\_TaxID=3352;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99408257; PubMed=10480380;  
 RA Li L., Osakabe Y., Joshi C.P., Chiang V.L.,  
 RT "Secondary xylem-specific expression of caffeoyl-coenzyme A 3-O-  
 RT methyltransferase plays an important role in the methylation pathway  
 RT associated with lignin biosynthesis in loblolly pine."  
 RL Plant Mol. Biol. 40:555-565(1999).  
 DR EMBL: AF098159; AAF00086.1; -;  
 KW Transferase; Methyltransferase.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA: 1164 MW: BC604447E4DDC2D5 CRC64;

Query Match 41.5%; Score 17; DB 10; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 7.3e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0.  
 OY 4 KELEF 8  
 DB 5 KELEF 9  
 ID 090QF8 PRELIMINARY; PRT: 12 AA.  
 AC 090QF8;  
 DT 01-MAY-2000 (TREMBLER, 13, Created)  
 DT 01-MAY-2000 (TREMBLER, 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLER, 13, Last annotation update)  
 DE CAFFEYL-COA O-METHYLTRANSFERASE (FRAGMENT).  
 OS Coffea arabica (Coffea arabica).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferales; Pinaceae; Pinus.  
 NCBI\_TaxID=3352;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99408257; PubMed=10480380;  
 RA Li L., Osakabe Y., Joshi C.P., Chiang V.L.,  
 RT "Secondary xylem-specific expression of caffeoyl-coenzyme A 3-O-  
 RT methyltransferase plays an important role in the methylation pathway  
 RT associated with lignin biosynthesis in loblolly pine."  
 RL Plant Mol. Biol. 40:555-565(1999).  
 DR EMBL: AF098159; AAF00086.1; -;  
 KW Transferase; Methyltransferase.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA: 1164 MW: BC604447E4DDC2D5 CRC64;

OY 1 VLAKELK 7  
1 1 1 1  
DB 6 VAAAEVK 12

## RESULT 10

ID P82431 PRELIMINARY: PRT: 15 AA.  
AC P82431;  
DT 01-JUN-2000 (TREMBLrel. 14, Created)  
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE 100 KDA CELL WALL PROTEIN (FRAGMENT).  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;  
OC Asparagales; Ranunculales I; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]  
RP SEQUENCE.  
RC STRAIN:CV. PETIT HAVANA;  
RA Blandin A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
RA Polasick P., Bolwell G.P.;  
RT "Ribosome study of secondary cell wall proteins from transformed  
tobacco culture".  
RT Plants 0:0-0(2000).  
CC -1 SUBCELLULAR LOCATION: CELL WALL.  
CC -1 TISSUE SPECIFICITY: XYLEM.  
KM CELL WALL.  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA: 1694 MW: 5F3B8D2E48187626 CRC64:

Query Match 41.5%; Score 17; DB 10; Length 15;  
Best Local Similarity 57.1%; Pred. No. 8.9e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VLAKELK 7  
1 1 1 1  
DB 3 VKKKDLK 9

## RESULT 11

ID 09HAD3 PRELIMINARY: PRT: 8 AA.  
AC 09HAD3;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE LIM DOMAIN ONLY 1 PROTEIN (FRAGMENT).  
GN LMOL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eultheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RA Brueckmann T., Winterpacht A., Hanneke T., Schmidt E.R., Zabel B.U.;  
RT "Human PAC clone RPCLP/04K0381 (pD3.781K3), sequenced in DHP project  
(Comparative Sequencing of a 1 Mb Region in Man (Chromosome 11p15) and  
Mouse (Chromosome 7))".  
RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RL EMBL: AJ277661; CAC14573.1;  
DR NON\_TER 8 8  
FT SEQUENCE 8 AA: 980 MW: F3AB133A3A32C696 CRC64:

Query Match 39.0%; Score 16; DB 4; Length 8;  
Best Local Similarity 80.0%; Pred. No. 5.6e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLAKELK 5  
1 1 1 1  
DB 3 VLKKE 7

## RESULT 12

ID P83160 PRELIMINARY: PRT: 10 AA.  
AC P83160;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE RUBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN (EC 4.1.1.39) (RUBISCO  
SMALL SUBUNIT) (FRAGMENT).  
OS Anabaena sp. (strain L31).  
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.  
OX NCBI\_TaxID=29412;  
RN [1]  
RP SEQUENCE.  
RA Apte S.K., Uhlemann E., Schmidt R., Alendort K.;  
RL Submitted (OCT-2001) to the Swiss Protein Data Bank  
CC -1 FUNCTION: RUBISCO CATALYZES THE PRIMARY EVENT IN PHOTOSYNTHETIC  
RUBULOSE 1,5-BISPHOSPHATE CARBOXYLASE REACTION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF  
THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH  
CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME  
CC ACTIVE SITE.  
CC -1 CATALYTIC ACTIVITY: D-RUBULOSE 1,5-BISPHOSPHATE + CO(2) = 2 3-  
CC PHOSHO-D-GICERATE.  
CC -1 PROSTHETIC ACTIVITY: D-RUBULOSE 1,5-BISPHOSPHATE + O(2) = 3-  
CC PHOSHO-D-GICERATE + 2-PHOSPHOGLYCOLATE.  
CC -1 SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.  
CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -1 SYNTACTIC: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.  
KM Photosynthesis: Carbon dioxide fixation; Photorespiration; Lyase;  
KM NON\_TER 10 10  
FT SEQUENCE 10 AA: 1322 MW: BB4E2D0B13276731 CRC64:

Query Match 39.0%; Score 16; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 1e+04;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 VLAKELK 8  
1 1 1 1  
DB 4 LPKERRY 10

## RESULT 13

ID 070580 PRELIMINARY: PRT: 10 AA.  
AC 070580;  
DT 01-AUG-1998 (TREMBLrel. 07, Created)  
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE CARBONIC ANHYDRASE III (FRAGMENT).  
GN CAR3 OR CAR5 OR CA3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eultheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Swiden J., Smith H., Morrison K., Edwards Y.;  
RT "Sequence comparisons and functional studies of the proximal promoter  
of the carbonic anhydrase 3 (CA3) gene".  
RL Gene 214:157-165(1999).  
DR EMBL: AJ006474; CAA07057.1;  
DR MGD: MGI:1351477; Car3.  
DR MGD: MGI:88270; Car3.  
DR NON\_TER 10 10  
FT SEQUENCE 10 AA: 1105 MW: 567FE71ADC37B13 CRC64:

Query Match 39.0%; Score 16; DB 11; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 1e+04; 0;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAKE 5  
 :|||  
 DB 1 MAKE 4

OY 2 LAKE 5  
 :|||  
 DB 1 MAKE 4  
 Search completed: August 21, 2002, 15:31:00  
 Job time: 209 sec

## RESULT 14

O9EU23 PRELIMINARY; PRT: 11 AA.  
 ID O9EU23  
 AC O9EU23 01-MAR-2001 (TREMBLER, 16, Created)  
 DT 01-MAR-2001 (TREMBLER, 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBLER, 16, Last annotation update)  
 DE RIBOSOME BINDING FACTOR A (FRAGMENT).  
 GN RBFA.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-10490;  
 RA Hedegaard J., Kristensen J.E., Nakamura Y., Sperling-Petersen H.U.,  
 Mortensen K.K.;  
 RT "Sequence of the infB gene from Escherichia coli strain 10489 and  
 10490.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ132862; CAC20133.1;  
 FT NON\_TER 11  
 SO SEQUENCE 11 AA; 1319 MW; 68234CFE740879CB CRC64;

Query Match 39.0%; Score 16; DB 2; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAKE 5  
 :|||  
 DB 1 MAKE 4

## RESULT 15

O60842 PRELIMINARY; PRT: 11 AA.  
 ID O60842  
 AC O60842 01-AUG-1998 (TREMBLER, 07, Created)  
 DT 01-AUG-1998 (TREMBLER, 07, Last sequence update)  
 DT 01-AUG-1998 (TREMBLER, 19, Last annotation update)  
 DE CARBONIC ANHYDRASE (FRAGMENT).  
 GN CA3.  
 OS Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sowden J., Smith H., Morrison K., Edwards Y.;  
 RT "Sequence comparisons and functional studies of the proximal promoter  
 of the carbonic anhydrase 3 (CA3) gene.";  
 RL Gene 214:157-165(1999).  
 DR EMBL: AJ006473; CAA07056.1;  
 FT NON\_TER 11  
 SO SEQUENCE 11 AA; 1293 MW; 7DB6AF84CB58637B CRC64;

Query Match 39.0%; Score 16; DB 4; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;